

A matched filter decomposition of fMRI into resting and task components*

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Abstract. The human brain exhibits dynamic interactions among brain regions when responding to stimuli and executing tasks, which can be recorded using functional magnetic resonance imaging (fMRI). Functional MRI signals collected in response to specific tasks consist of a combination of task-related and spontaneous (task-independent) activity. By exploiting the highly structured spatiotemporal patterns of resting state networks, this paper presents a matched-filter approach to decomposing fMRI signals into task and resting-state components. To perform the decomposition, we first use a temporal alignment procedure that is a windowed version of the brainsync transform to synchronize a resting template to the brain's response to tasks. The resulting 'matched filter' removes the components of the fMRI signal that can be described by resting connectivity, leaving the portion of brain activity directly related to tasks. We present a closed-form expression for the windowed synchronization transform that is used by the matched filter. We demonstrate performance of this procedure in application to motor task and language task fMRI data. We show qualitatively and quantitatively that by removing the resting activity, we are able to identify task activated regions in the brain more clearly. Additionally, we show improved prediction accuracy in multivariate pattern analysis when using the matched filtered fMRI data.

1 Introduction

The human brain exhibits intricate, complex, and dynamic interactions among functional regions. Functional MRI (fMRI) recorded during rest or task activity can be used to image these interactions. Researchers have typically focused on finding large-scale network organization either in resting-state [9] or event-related task paradigms [2]. However, It has been shown that, the signal component in fMRI data that is predominantly observed during rest due to body regulation, as well as in the default mode network, is active not only during wakeful rest and mind-wandering but also during goal-oriented tasks [11]. A number of neuroimaging studies have shown that brain activity during rest may have even higher power when performing specific tasks, those involving cognitive challenges [3]. Separating event-related and spontaneous components in fMRI recordings

* This work is supported by the following grants: R01-NS074980, W81XWH-18-1-0614, R01-NS089212, and R01-EB026299.

can potentially improve detection of task-related components as well as offer new insights into the interaction between intrinsic brain activity [10] and the brain’s response to external stimulation and challenges.

Given the task design, a generalized linear regression (GLM) model is often fit to the fMRI time courses, which leads to a statistical parametric map of brain regions associated with tasks. Alternatively, independent component analysis (ICA) based methods extract task-associated components [13]. However, statistical power can be limited due to the limited number of samples and trials during fMRI acquisition and the presence of non-task-related components. Due to the finite length of the acquisition, the design blocks may correlate with these unrelated spontaneous components. Another confound is that some of the spontaneous components may be anti-correlated (e.g. the default mode network) with a task and show significance even though they are not directly involved in responding to the task [11]. Filtering out spontaneous components from task fMRI recordings can therefore potentially improve the statistical power of task-related studies.

We exploit the learned resting state connectivity patterns between brain networks to identify and remove on-going brain activity unconnected to the task from fMRI signals. Specifically, we describe a method that decomposes fMRI signals into an on-going or ‘resting’ component, the component which has connectivity (correlation) patterns similar to that observed during rest, and a residual ‘task’ component, the component which is related to tasks and differs in its dynamics and connectivity from resting activity. This decomposition allows us to study the brain’s functional dynamics, at a high spatial as well as temporal resolution. For this purpose, we first learn a ‘resting template’ based on resting fMRI collected from a control group. Next, we develop a windowed extension of the brainsync transform to perform a matched filtering of fMRI data using this template. The modified transform is then applied to perform a matched filtering of the task fMRI data, as explained below. Results in application to task data from the Human Connectome Project (HCP) are presented.

2 Materials and methods

As input, we assume that the resting state fMRI data has been preprocessed and mapped to the grayordinate system that represents fMRI data on a tessellated surface of the cerebral cortex and volumetric subcortical gray matter [5]. The cortical surfaces for each subject are also assumed to be aligned and resampled onto a common mesh. The grayordinate representation of fMRI data for each subject is represented as a matrix F of size $T \times V$, where V is the number of vertices in the cortical mesh plus the number of subcortical voxels and T is the number of time points, respectively. Hence the corresponding columns in F represents the time-series at homologous locations in the brains. The data vectors in each column are normalized to have zero mean and unit norm. We want to decompose fMRI data into two components as follows:

$$F(t, x) = S(t, x) + D(t, x) \quad (1)$$

where $F(t, x)$ is the fMRI signal at location x and time point t , $S(t, x)$ is the resting component and $D(t, x)$ is the task component (Fig. 1 (a)). We perform this decomposition by designing a matched filter which ensures that $S(t, x)$ has functional connectivity (correlation) matched to that observed during rest. This is done by first generating a template from resting state fMRI data of short time-length and then matching it to the original data $F(t, x)$ in a sliding window manner using the brainsync transform. Brainsync is an orthogonal transform [7] that can be used for comparison of fMRI scans that are collected during rest or task paradigms across different subjects. This transform finds an orthogonal matrix that ‘synchronizes’ fMRI data between two subjects, such that the time series at homologous locations in the two brains become approximately equal.

2.1 Resting template generation

We considered 40 normal subjects, each with $Tr \times V$ data matrices, from the HCP database ($Tr = 1200$ and $V = 91,282$ for HCP resting fMRI data) and synchronized them to a representative subject using the brainsync transform. The representative subject was chosen to be the one that has the least root mean square (RMS) distance to the rest of the subjects [7]. The synchronized data was then averaged over subjects to generate a single average dataset of size $Tr \times V$. This average data set was then reduced to dimension $T = 21$ by projection onto the temporal singular vectors corresponding to the 21 largest singular values to capture the significant variations in the resting template, as illustrated in Fig. 1 (b). The reduced dimension $T = 21$ was chosen based on the spread of the singular values of the data matrix, as illustrated in Fig. 1 (b). This

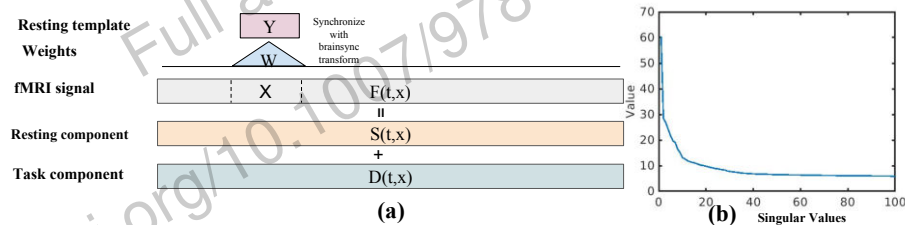


Fig. 1. (a) Schematic of the proposed method; (b) Singular values for a typical resting state fMRI scan.

template Y , as shown in Fig. 1 (a), largely retains the correlation structure of the original data because of the reduced-rank optimality properties of the truncated SVD. Next, we develop a weighted extension of the brainsync transform to use this template for the proposed matched filtering.

2.2 Windowed brainsync transform

We use the resting template pattern Y to identify and remove the components in the task data which exhibit the same connectivity (correlation) pattern as the template. In order to estimate the resting component we synchronize the template Y to a windowed (with arbitrary window W) data segment X at each time point of the target fMRI data F (Fig. 1). For this purpose, we solve the orthogonal Procrustes problem with a weighting defined by W .

Let $X_{T \times V} = \{x_{ij}\}$ denote a length- T fMRI data segment in $F(t, x)$ centered at some given time point, $Y_{T \times V} = \{y_{ij}\}$ denote the resting-template with the same length, and $O_{T \times T}$ denote the orthogonal transform which transforms Y to match X . We assume the resting component of F has the same correlation structure as the template and can therefore be approximated using an orthogonal transformed version of Y [7]. We include a scaling factor α to scale the resting-template signal and W , a diagonal matrix representing the window centered on the current time point. The scaling factor α and the orthogonal transform O are obtained by minimizing the energy

$$E = \|W(\alpha OY - X)\|_F^2 = \sum_{n=1}^V \|W(\alpha O\mathbf{y}_n - \mathbf{x}_n)\|^2$$

subject to the orthogonality constraints on O : $\sum_{k=1}^T O_{ki}O_{kj} - \delta_{ij} = 0$, where δ_{ij} is the Kronecker delta. Here, \mathbf{y}_n and \mathbf{x}_n denote columns of Y and X , centered on the current time sample and of length equal to the dimension of W , respectively. To enforce the orthogonality constraint, we define a symmetric Lagrange multiplier $l_{ij} = l_{ji}$ and the Lagrangian cost G as:

$$G = \sum_{i,j=1}^T l_{ij} \left(\sum_{k=1}^T O_{ki}O_{kj} - \delta_{ij} \right) + \sum_{n=1}^V \sum_{i=1}^T W_i^2 \left(\sum_{j=1}^T \alpha O_{ij} y_{jn} - x_{in} \right)^2$$

To find O_{ij} , we take derivatives of G w.r.t. O_{ij} and equate it to zero and follow the simplifying steps in [8]. This leads to a closed form expression for O as follow. Define the weighted correlation matrix $R = W^2XY^T$ and its SVD $R = B\Lambda A^T$. The orthogonal matrix is then given simply by:

$$O = BA^T. \quad (2)$$

Now to find α , we compute

$$\begin{aligned} \frac{\partial E}{\partial \alpha} &= 2 \sum_{n=1}^V (W(\alpha O\mathbf{y}_n - \mathbf{x}_n))^T W O \mathbf{y}_n = 0 \\ \alpha &= \frac{\text{trace}((WX)^T(WOY))}{\text{trace}((WOY)^T(WOY))}. \end{aligned} \quad (3)$$

Finally, the estimated resting component at a particular time t is given by αOY evaluated at the central time point and the task component is obtained by

subtracting the resting component from the original data. This procedure is performed in a sliding window manner to construct the entire resting component $S(t, x)$ as well as the task component $D(t, x)$ as depicted in Fig. 1 (a). We chose a triangle window W for this analysis in order to emphasize the current time point and linearly weight neighboring time points in the sliding window analysis.

3 Applications and experimental results

In order to explore the performance of our matched filtering, we applied the filter to minimally preprocessed (ICA-FIX denoised) resting and task fMRI data from 40 independent subjects (all right-handed, age 26-30, 16 male and 24 female), which are publicly available from HCP [1, 5]. The resting template was built using the method described in Sec. 2.1 and the matched filtering was performed using the weighted brainsync transform as explained in Sec. 2.2.

3.1 Motor task

The motor task in the HCP project involves right versus left toe (foot block) and finger (hand block) movements, as well as tongue movement (tongue block). While this task usually presents a clear contrast, even without our matched fil-

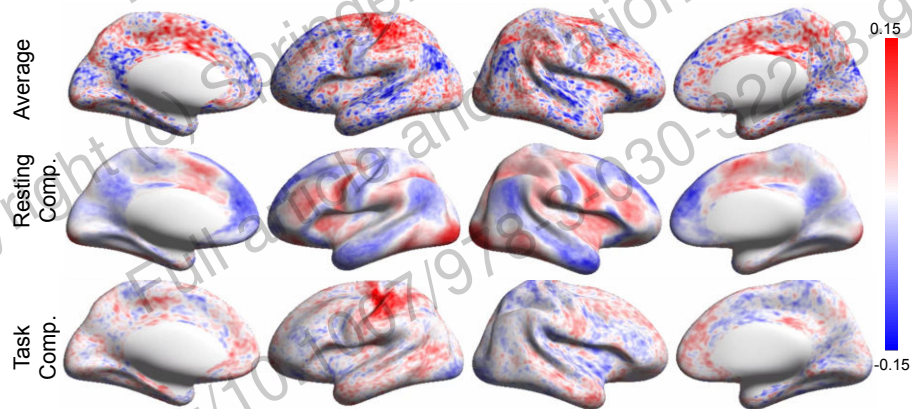


Fig. 2. The fMRI signal at a single time point during the ‘right hand’ block in the motor task fMRI data. Top row shows the direct average of the signal over 40 subjects; the second row shows the extracted resting component; and the bottom row shows the extracted task component.

tering, here we use it for illustrative purpose, aiming at demonstration of the ability of the matched filter to distinguish resting and task components. Matched filtering was performed for each member of the subject population. The population average signal at a single time point in the ‘right-hand’ block is shown in

Fig. 2. It can be seen that while the direct average signal clearly shows the hand associated region, there is also a large amount of activity in other areas of the brain. The estimated resting component shown in the middle row clearly shows the resting-related activity which forms a significant part of the signal power, but does not contain significant task-related activity. The task component from the decomposition retains a relatively large signal in the left somatomotor cortex while the activity elsewhere in the brain is significantly reduced.

3.2 Language task

The language task in the HCP data contains two design blocks. One block is an auditory story presentation with comprehension questions and the second block includes a set of math problems [1]. Similar to Sec. 3.1, the matched filtering

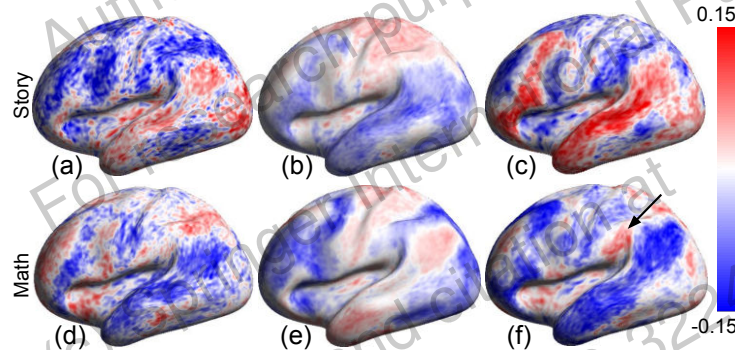


Fig. 3. The fMRI at a single time point during the ‘story’ block (a-c) and ‘math’ block (d-f) in the language task; (a,d) direct average over subjects; (b,e) resting component and (c,f) task components extracted using matched filtering.

was performed and the signal was averaged over subjects and displayed for two time points as described in the caption of Fig. 3. For the ‘story’ block, the activation in Broca’s and Wernicke’s areas is much clearer after subtraction of the estimated resting component. Also, stronger activation of the anterior temporal lobe associated with language comprehension and processing was observed. Similarly, for the ‘math’ block, Fig. 3 (f) demonstrates that the angular gyrus (indicated by an arrow in Fig. 3 (f)) that is associated with arithmetic processing is clear in the task component, while it is more difficult to discern without the matched filtering (Fig. 3 (d)).

We also computed the signal averaged over the time samples for one design block of the story task. We see in Fig. 4 that the language areas are much more clearly delineated in the average task component. It should be noted that the results of the standard GLM analysis presented in [1] and other HCP publications are similar to our average signal results. To quantitatively evaluate the contrast

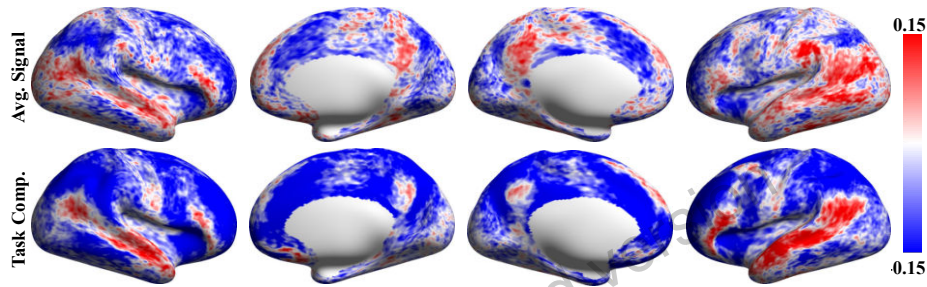


Fig. 4. The fMRI signal averaged over the ‘story’ block in the language task: (top row) direct average; (bottom row) averaged task components extracted using the proposed matched filtering.

enhancement in the task data, we first identified the points in the grayordinates that are associated with the tasks. For this purpose, we averaged the z-score maps for each task as provided by the HCP project, and computed the average over the 40 subjects [1]. The average z-score maps were converted to p-value maps and corrected for multiple comparisons using Benjamini-Hochberg FDR correction. The task associated regions were generated by choosing a threshold of $p < 0.05$. Next, we computed the difference between the average signal in these task associated regions and the average signal of the rest in the brain during the task blocks. This statistic was computed for the task fMRI data-sets for each of the 40 subjects and the means and variances of the statistic across subjects are tabulated in Table 1. Statistical testing using a ranksum test showed that there is a significant increase in contrast in the task component for all tasks in all cases ($p\text{-val} < 1e-6$) after matched filtering.

Task (subtask)	Original	Match filtered	p-value.
Motor (hand)	0.10 (0.04)	0.16 (0.02)	3e-7
Motor (right foot)	0.09 (0.03)	0.11 (0.02)	4e-7
Motor (tongue)	0.10 (0.04)	0.14 (0.03)	1e-11
Language (story)	0.06 (0.05)	0.18 (0.02)	8e-13
Language (math)	0.04 (0.06)	0.11 (0.03)	1e-6

Table 1. Differences in average signals in task associated and non-associated areas in the brain. The mean and variances of the observed contrast is reported.

3.3 MVPA analysis of language data

To further explore the applicability of the matched filter in task studies, we also performed a multivariate pattern analysis (MVPA) of the language data for 40 subjects from the HCP dataset. We ignored the data between task blocks. We

performed MVPA analysis [6] of story vs math blocks with and without the proposed filtering.

The MVPA analysis uses a Support Vector Machine to classify the annotated time series fMRI data. Specifically, we used Support Vector Classification (SVC) [4] with $C = 1$ and a linear kernel. We performed 5-fold cross-validation (CV), which involves iteratively training the SVM classifier using 80% of the time series and its annotations and making predictions of the annotation for the remaining 20% of the time series. The mean (std) CV accuracy for story vs math paradigm, for the original data was 0.7815(0.1232) and for the matched filtered data was 0.8054(0.1423). Each of the ‘story’ and ‘math’ tasks is subdivided into ‘present’, ‘question’ and ‘response’ sub-blocks. Next, we considered the six sub-blocks as separate labels for the time series and performed multi-class SVM analysis (one vs one classification). The CV accuracy in this case, for the original data, was 0.7423(0.1026) and for the matched filtered data, was 0.8423(0.0976).

4 Discussion and conclusion

We present a matched filter approach for decomposition of fMRI data into task-independent and task-related components. By removing the confounding non-task-related on-going (or ‘resting’) activity from the fMRI data, the contrasts in the task data are enhanced. Previous studies have shown that subtracting resting activity as a baseline can reduce or eliminate the effects related to the task function [12]. In contrast, in our approach, the component being subtracted was generated by leveraging the brainsync transform. This method involves application of an orthogonal transform and scaling of the template to the original signal, rather than simple subtraction. Therefore, the proposed approach might be more suitable for removing non-task-related activity from task fMRI recordings.

In the current work, a common factor α is applied and one matched filter is designed for the entire resting-state network. However, different components representing sub-networks within the resting state might have different contributions as well as individual variation over time in the task data. An alternative approach could be to design separate matched filters for different sub-networks within the resting state network. We will explore this approach in the future.

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